

SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Tyrosine phosphorylation of p27Kip1

<130> 22250

<150> EP03024165.7

<151> 2003-10-20

<160> 25

<170> PatentIn version 3.2

<210> 1

<211> 597

<212> DNA

<213> Homo sapiens

<400> 1

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ttaacccggg acttggagaa gcactgcaga gacatggaag aggcgagcca gcgcaagtgg 180

aatttcgatt ttcagaatca caaaccctta gaggcaagt acgagtggca agaggtggag 240

aagggcagct tgcccagtt ctactacaga ccccccggc cccccaagg tgcctgcaag 300

gtgccggcgc aggagagcca ggatgtcagc gggagccgcc cggcggcgcc tttaattggg 360

gctccggcta actctgagga cacgcatttgc gtggacccaa agactgatcc gtcggacagc 420

cagacggggt tagcggagca atgcgcagga ataaggaagc gacctgcaac cgacgattct 480

tctactcaaa acaaagagc caacagaaca gaagaaaatg tttcagacgg ttccccaaat 540

gccggttctg tggagcagac gcccaagaag cctggcctca gaagacgtca aacgtaa 597

<210> 2

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<213> Homo sapiens

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Asp Ala Arg Gln Ala Glu His Pro Lys Pro Ser Ala Cys Arg Asn Leu
20 25 30

Phe Gly Pro Val Asp His Glu Glu Leu Thr Arg Asp Leu Glu Lys His
 35 40 45

Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe
 50 55 60

Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu
 65 70 75 80

Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys
 85 90 95

Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Ser
 100 105 110

Arg Pro Ala Ala Pro Leu Ile Gly Ala Pro Ala Asn Ser Glu Asp Thr
 115 120 125

His Leu Val Asp Pro Lys Thr Asp Pro Ser Asp Ser Gln Thr Gly Leu
 130 135 140

Ala Glu Gln Cys Ala Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser
 145 150 155 160

Ser Thr Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp
 165 170 175

Gly Ser Pro Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly
 180 185 190

Leu Arg Arg Arg Gln Thr
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<210> 3
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 tgcatccagg aggccccgtga gcgatggAAC ttgcactttg tcaccgagac accactggag 180

ggtgacttcg cctgggagcg tgtgcggggc cttggcctgc ccaagctcta cttccacg	240
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ctgctgcagg ggacagcaga ggaagaccat gtggacctgt cactgtcttg tacccttgc	360
cctcgctcag gggagcaggc tgaagggtcc ccaggtggac ctggagactc tcagggtcga	420
aaacggcggc agaccagcat gacagatttc taccactcca aacgcccggct gatcttctcc	480
aagaggaagc cctaa	495

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Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln Glu Ala Arg Glu Arg		
35	40	45

Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu Glu Gly Asp Phe Ala		
50	55	60

Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys Leu Tyr Leu Pro Thr			
65	70	75	80

Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly Arg Arg Pro Gly		
85	90	95

Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu Glu Asp His Val Asp		
100	105	110

Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser Gly Glu Gln Ala Glu		
115	120	125

Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly Arg Lys Arg Arg Gln		
130	135	140

Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg Arg Leu Ile Phe Ser
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Lys Arg Lys Pro

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 gagctgagcc gcgagctgca ggcccgccctg gccgagctga acgcccagga ccagaaccgc 180
 tgggattacg acttccagca ggacatgccc ctgcggggcc ctggacgcct gcagtgacc 240
 gaagtggaca gcgactcggt gcccgcgttc taccgcgaga cgggtcaggt ggggcgtgc 300
 cgcctgctgc tggcgcccg gcccgtcgcg gtcgcgggtgg ctgtcagccc gcccctcgag 360
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 gtcccgcccc cggcgccac cccggggccca gtcccggtcc tggctccagc cccggggcccg 480
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 caagagagcg ccgagcaggg cgcgaaaccag gggcagcgcg gccaggagcc tctcgctgac 720
 cagctgcact cggggatttc gggacgtccc gcggccggca cgcggccgc cagcgccaaac 780
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<400> 6

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Ala Arg Gly Thr Phe Pro Val Leu Val Arg Thr Ser Ala Cys Arg Ser
20 25 30

Leu Phe Gly Pro Val Asp His Glu Glu Leu Ser Arg Glu Leu Gln Ala
35 40 45

Arg Leu Ala Glu Leu Asn Ala Glu Asp Gln Asn Arg Trp Asp Tyr Asp
50 55 60

Phe Gln Gln Asp Met Pro Leu Arg Gly Pro Gly Arg Leu Gln Trp Thr
65 70 75 80

Glu Val Asp Ser Asp Ser Val Pro Ala Phe Tyr Arg Glu Thr Val Gln
85 90 95

Val Gly Arg Cys Arg Leu Leu Leu Ala Pro Arg Pro Val Ala Val Ala
100 105 110

Val Ala Val Ser Pro Pro Leu Glu Pro Ala Ala Glu Ser Leu Asp Gly
115 120 125

Leu Glu Glu Ala Pro Glu Gln Leu Pro Ser Val Pro Val Pro Ala Pro
130 135 140

Ala Ser Thr Pro Pro Pro Val Pro Val Leu Ala Pro Ala Pro Ala Pro
145 150 155 160

Ala Pro Ala Pro Val Ala Ala Pro Val Ala Ala Pro Val Ala Val Ala
165 170 175

Val Leu Ala Pro
180 185 190

Ala Pro Val Ala Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
195 200 205

Ala Pro Ala Pro Ala Pro Ala Pro Asp Ala Ala Pro Gln Glu Ser Ala
210 215 220

Glu Gln Gly Ala Asn Gln Gly Gln Arg Gly Gln Glu Pro Leu Ala Asp
225 230 235 240

Gln Leu His Ser Gly Ile Ser Gly Arg Pro Ala Ala Gly Thr Ala Ala
245 250 255

Ala Ser Ala Asn Gly Ala Ala Ile Lys Lys Leu Ser Gly Pro Leu Ile
260 265 270

Ser Asp Phe Phe Ala Lys Arg Lys Arg Ser Ala Pro Glu Lys Ser Ser
275 280 285

Gly Asp Val Pro Ala Pro Cys Pro Ser Pro Ser Ala Ala Pro Gly Val
290 295 300

Gly Ser Val Glu Gln Thr Pro Arg Lys Arg Leu Arg
305 310 315

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<400> 8
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<400> 9
gcttgcccgaa gttctatttc agaccccccgc gg

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<210> 10
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ccgcgggggt ctgaaataga actcgggcaa gc

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<400> 13

cccttagagg gcaagttcga gtggcaagag

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<400> 17
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<400> 18
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<400> 19
gcatatgggg cagcagcctg g

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<400> 20
gcaggcggat ccgacgggcc

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<210> 21
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<400> 21

Glu Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro
1 5 10 15

<210> 22
<211> 12
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<400> 22

Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro
1 5 10

<210> 23

<211> 10

<212> PRT

<213> Homo sapiens

<400> 23

Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg
1 5 10

<210> 24

<211> 8

<212> PRT

<213> Homo sapiens

<400> 24

Pro Glu Phe Tyr Tyr Arg Pro Pro
1 5

<210> 25

<211> 6

<212> PRT

<213> Homo sapiens

<400> 25

Glu Phe Tyr Tyr Arg Pro
1 5